SEQUENCE LISTING

<110> Bartel, Paul L.
Tavtigian, Sean V.
Myriad Genetics, Inc.

<120> MMSC1 - An MMAC1 Interacting Protein

<130> MMSC1 Gene

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<150> US 60/071,861
<151> 1998-01-20

<160> 65

<170> PatentIn Ver. 2.0

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Met
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cct gaa aat cct gct aca gat aaa ctg cag gtg ctg cag gta ctt gat 165
Pro Glu Asn Pro Ala Thr Asp Lys Leu Gln Val Leu Gln Val Leu Asp
5 10 15

cgc ctg aaa atg aaa ttg cag gag aag ggt gac acg tcg cag aat gag 213
Arg Leu Lys Met Lys Leu Gln Glu Lys Gly Asp Thr Ser Gln Asn Glu
20 25 30

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aag tta tct atg ttt tat gag aca cta aag agt cct ctc ttc aac cag   261
Lys Leu Ser Met Phe Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn Gln
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ata ctc aca ctt cag cag tcc atc aag caa ctg aag ggt caa ctc aac   309
Ile Leu Thr Leu Gln Gln Ser Ile Lys Gln Leu Lys Gly Gln Leu Asn
 50                  55                  60                  65

cat ata ccc tca gat tgt tca gcc aac ttt gat ttt tct agg aaa ggt   357
His Ile Pro Ser Asp Cys Ser Ala Asn Phe Asp Phe Ser Arg Lys Gly
                 70                  75                  80

ttg tta gtg ttc aca gat ggt tcc att act aat gga aat gtc cac agg   405
Leu Leu Val Phe Thr Asp Gly Ser Ile Thr Asn Gly Asn Val His Arg
             85                  90                  95

ccc tct aat aac tcg act gta tct ggg tta ttt ccg tgg acc ccg aag   453
Pro Ser Asn Asn Ser Thr Val Ser Gly Leu Phe Pro Trp Thr Pro Lys
        100                 105                 110

ttg gga aat gaa gac ttt aac tca gtc att caa cag atg gct cag ggc   501
Leu Gly Asn Glu Asp Phe Asn Ser Val Ile Gln Gln Met Ala Gln Gly
    115                 120                 125

cgg caa att gaa tat ata gat ata gaa cgg cct tca act gga ggc ctt   549
Arg Gln Ile Glu Tyr Ile Asp Ile Glu Arg Pro Ser Thr Gly Gly Leu
130                 135                 140                 145

gga ttc agt gtg gtg gcc ctc aga agt caa aat ctc gga aaa gtt gat   597
Gly Phe Ser Val Val Ala Leu Arg Ser Gln Asn Leu Gly Lys Val Asp
                150                 155                 160

atc ttc gtg aag gat gtc cag cca ggg agt gta gca gac agg gat caa   645
Ile Phe Val Lys Asp Val Gln Pro Gly Ser Val Ala Asp Arg Asp Gln
            165                 170                 175

aga tta aag gaa aat gat caa ata ttg gcc att aat cac acg cca ttg   693
Arg Leu Lys Glu Asn Asp Gln Ile Leu Ala Ile Asn His Thr Pro Leu
        180                 185                 190

gat cag aac att tcc cat cag caa gca att gca tta tta caa caa acc   741
Asp Gln Asn Ile Ser His Gln Gln Ala Ile Ala Leu Leu Gln Gln Thr
    195                 200                 205

act gga tct ttg aga ctg att gtg gcc agg gaa cca gtc cac aca aaa   789
Thr Gly Ser Leu Arg Leu Ile Val Ala Arg Glu Pro Val His Thr Lys
210                 215                 220                 225

agc agt act tct agc agc cta aat gat aca act ctg cct gaa aca gtt   837
Ser Ser Thr Ser Ser Ser Leu Asn Asp Thr Thr Leu Pro Glu Thr Val
                230                 235                 240

tgt tgg ggc cat gtt gaa gag gtt gag ctc att aat gat ggc tct gga   885
Cys Trp Gly His Val Glu Glu Val Glu Leu Ile Asn Asp Gly Ser Gly
            245                 250                 255

cta ggt ttt gga ata gtt gga gga aaa aca agt ggc gtg gtt gtg agg   933
Leu Gly Phe Gly Ile Val Gly Gly Lys Thr Ser Gly Val Val Val Arg
        260                 265                 270

act ata gtt cct gga gga tta gca gat cga gat gga aga ctc cag aca   981
Thr Ile Val Pro Gly Gly Leu Ala Asp Arg Asp Gly Arg Leu Gln Thr
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ggg gac cac atc ttg aag att ggt ggc aca aac gtg cag gga atg acc   1029
Gly Asp His Ile Leu Lys Ile Gly Gly Thr Asn Val Gln Gly Met Thr
290                 295                 300                 305

agt gag caa gtt gca caa gtt cta agg aac tgt ggg aat tca gtc agg   1077
Ser Glu Gln Val Ala Gln Val Leu Arg Asn Cys Gly Asn Ser Val Arg
                310                 315                 320

atg ctc gtt gct aga gat cca gct ggt gac att tca gtc acc ccc cct   1125
Met Leu Val Ala Arg Asp Pro Ala Gly Asp Ile Ser Val Thr Pro Pro
            325                 330                 335

gcc cct gca gcc tta cct gtt gcc ctg cct act gta gcc agc aag ggc   1173
Ala Pro Ala Ala Leu Pro Val Ala Leu Pro Thr Val Ala Ser Lys Gly
        340                 345                 350

cct ggt tct gac agt tct ctt ttt gaa act tat aat gtt gag ctt gtg   1221
Pro Gly Ser Asp Ser Ser Leu Phe Glu Thr Tyr Asn Val Glu Leu Val
    355                 360                 365

aga aaa gat ggg cag agt ctt gga att aga att gtt ggc tat gtt gga   1269
Arg Lys Asp Gly Gln Ser Leu Gly Ile Arg Ile Val Gly Tyr Val Gly
370                 375                 380                 385

aca tct cat aca ggg gaa gct tca ggg att tat gtg aaa agt gta ata   1317
Thr Ser His Thr Gly Glu Ala Ser Gly Ile Tyr Val Lys Ser Val Ile
                390                 395                 400

cct ggc agt gct gcg tac cac aat ggc cac att caa gtg aat gac aaa   1365
Pro Gly Ser Ala Ala Tyr His Asn Gly His Ile Gln Val Asn Asp Lys
            405                 410                 415

ata gtt gct gtc gat ggc gtg aac att cag ggt ttt gcc aac cat gat   1413
Ile Val Ala Val Asp Gly Val Asn Ile Gln Gly Phe Ala Asn His Asp
        420                 425                 430

gtt gtt gaa gta tta cga aat gca ggg cag gtg gta cac cta acc cta   1461
Val Val Glu Val Leu Arg Asn Ala Gly Gln Val Val His Leu Thr Leu
    435                 440                 445

gtt cga agg aag aca tcc tca tct act tct cca ctt gaa cca cct tca   1509
Val Arg Arg Lys Thr Ser Ser Ser Thr Ser Pro Leu Glu Pro Pro Ser
450                 455                 460                 465

gac aga gga act gtt gta gaa cca ctg aaa cca cca gct ctc ttt cta   1557
Asp Arg Gly Thr Val Val Glu Pro Leu Lys Pro Pro Ala Leu Phe Leu
                470                 475                 480

act gga gca gtg gaa act gaa act aat gtg gat ggt gaa gat gag gaa   1605
Thr Gly Ala Val Glu Thr Glu Thr Asn Val Asp Gly Glu Asp Glu Glu
            485                 490                 495

att aaa gaa aga att gat act tta aaa aat gac aac ata caa gcc tta   1653
Ile Lys Glu Arg Ile Asp Thr Leu Lys Asn Asp Asn Ile Gln Ala Leu
        500                 505                 510

gaa aaa ttg gaa aaa gtc cca gac tct cca gaa aat gag ctg aaa tcc   1701
Glu Lys Leu Glu Lys Val Pro Asp Ser Pro Glu Asn Glu Leu Lys Ser
    515                 520                 525

aga tgg gaa aac ctg ttg ggt cct gat tat gaa gta atg gtt gct act   1749
Arg Trp Glu Asn Leu Leu Gly Pro Asp Tyr Glu Val Met Val Ala Thr
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ttg gac aca cag att gca gat gat gct gag tta cag aaa tat tca aag   1797
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ctg ctg cct att cac act ctg agg ctt ggt gtg gaa gtg gat tcc ttt   1845
Leu Leu Pro Ile His Thr Leu Arg Leu Gly Val Glu Val Asp Ser Phe
            565                 570                 575

gat ggg cac cat tat att tct tca att gtt tct ggt ggt cct gtt gat   1893
Asp Gly His His Tyr Ile Ser Ser Ile Val Ser Gly Gly Pro Val Asp
        580                 585                 590

aca ttg ggt ctc cta cag cca gaa gat gag ctg ctt gag gtc aat ggc   1941
Thr Leu Gly Leu Leu Gln Pro Glu Asp Glu Leu Leu Glu Val Asn Gly
    595                 600                 605

atg cag ctt tat gga aaa tct cgc cga gaa gca gtc tcc ttt ctt aaa   1989
Met Gln Leu Tyr Gly Lys Ser Arg Arg Glu Ala Val Ser Phe Leu Lys
610                 615                 620                 625

gaa gtg cca ccc cct ttt act ttg gtt tgc tgt cgg agg ttg ttt gat   2037
Glu Val Pro Pro Pro Phe Thr Leu Val Cys Cys Arg Arg Leu Phe Asp
                630                 635                 640

gat gaa gct tct gta gat gaa cca agg cgc act gaa acc tct ctt cct   2085
Asp Glu Ala Ser Val Asp Glu Pro Arg Arg Thr Glu Thr Ser Leu Pro
            645                 650                 655

gag aca gag gtt gac cac aat atg gat gtc aat act gaa gaa gat gat   2133
Glu Thr Glu Val Asp His Asn Met Asp Val Asn Thr Glu Glu Asp Asp
        660                 665                 670

gat ggg gaa tta gca ctg tgg tcc cct gaa gtc aag att gtt gaa cta   2181
Asp Gly Glu Leu Ala Leu Trp Ser Pro Glu Val Lys Ile Val Glu Leu
    675                 680                 685

gta aaa gat tgt aaa ggt ttg gga ttc agc att ttg gat tac cag gac   2229
Val Lys Asp Cys Lys Gly Leu Gly Phe Ser Ile Leu Asp Tyr Gln Asp
690                 695                 700                 705

cct tta gat cct aca aga tca gtg att gtg atc cgc tcc ctg gta gca   2277
Pro Leu Asp Pro Thr Arg Ser Val Ile Val Ile Arg Ser Leu Val Ala
                710                 715                 720

gat ggt gta gca gaa aga agt ggg gga cta tta cct gga gac cgc ctg   2325
Asp Gly Val Ala Glu Arg Ser Gly Gly Leu Leu Pro Gly Asp Arg Leu
            725                 730                 735

gtc tca gtc aat gaa tac tgt ttg gac aac acc tca ctt gct gaa gct   2373
Val Ser Val Asn Glu Tyr Cys Leu Asp Asn Thr Ser Leu Ala Glu Ala
        740                 745                 750

gtg gaa ata ttg aaa gct gtg cca cca ggc cta gta cac ctt ggc atc   2421
Val Glu Ile Leu Lys Ala Val Pro Pro Gly Leu Val His Leu Gly Ile
    755                 760                 765

tgt aag cct ttg gtg gaa gat aat gaa gaa gaa agt tgt tat att tta   2469
Cys Lys Pro Leu Val Glu Asp Asn Glu Glu Glu Ser Cys Tyr Ile Leu
770                 775                 780                 785

cat tca agc agt aat gaa gac aag act gaa ttt tca gga aca att cat   2517
His Ser Ser Ser Asn Glu Asp Lys Thr Glu Phe Ser Gly Thr Ile His
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gat ata aat tca tct tta ata ctc gaa gca ccc aag gga ttt aga gat   2565
Asp Ile Asn Ser Ser Leu Ile Leu Glu Ala Pro Lys Gly Phe Arg Asp
            805                 810                 815

gaa cca tat ttt aaa gaa gaa ctt gtg gat gaa cca ttt cta gat ctg   2613
Glu Pro Tyr Phe Lys Glu Glu Leu Val Asp Glu Pro Phe Leu Asp Leu
        820                 825                 830

gga aag tct ttc cat tcc caa caa aaa gag ata gag caa agc aag gag   2661
Gly Lys Ser Phe His Ser Gln Gln Lys Glu Ile Glu Gln Ser Lys Glu
    835                 840                 845

gcc tgg gag atg cat gaa ttt ctg act cct aga ttg cag gaa atg gat   2709
Ala Trp Glu Met His Glu Phe Leu Thr Pro Arg Leu Gln Glu Met Asp
850                 855                 860                 865

gaa gaa aga gaa atg ctt gtt gat gaa gaa tat gag tta tat caa gat   2757
Glu Glu Arg Glu Met Leu Val Asp Glu Glu Tyr Glu Leu Tyr Gln Asp
                870                 875                 880

ccc tca cca tcc atg gag ttg tat ccc ttg tcg cac att caa gag gcc   2805
Pro Ser Pro Ser Met Glu Leu Tyr Pro Leu Ser His Ile Gln Glu Ala
            885                 890                 895

act cct gtg ccc tct gtg aat gaa ctt cac ttt ggt aca cag tgg ttg   2853
Thr Pro Val Pro Ser Val Asn Glu Leu His Phe Gly Thr Gln Trp Leu
        900                 905                 910

cat gat aat gaa cca tcc gag tct caa gag gca aga acc ggg agg act   2901
His Asp Asn Glu Pro Ser Glu Ser Gln Glu Ala Arg Thr Gly Arg Thr
    915                 920                 925

gtc tat tcc cag gag gca cag ccg tat ggc tat tgc cct gaa aat gtg   2949
Val Tyr Ser Gln Glu Ala Gln Pro Tyr Gly Tyr Cys Pro Glu Asn Val
930                 935                 940                 945

atg aaa gaa aat ttt gtc atg gag tcc cta cca tct gta cca tca act   2997
Met Lys Glu Asn Phe Val Met Glu Ser Leu Pro Ser Val Pro Ser Thr
                950                 955                 960

gaa gga aac agt caa caa ggc aga ttt gac gac ctg gaa aat ctt aat   3045
Glu Gly Asn Ser Gln Gln Gly Arg Phe Asp Asp Leu Glu Asn Leu Asn
            965                 970                 975

tca tta gca aaa act agt ctg gat tta ggc atg atc ccg aat gat gtc   3093
Ser Leu Ala Lys Thr Ser Leu Asp Leu Gly Met Ile Pro Asn Asp Val
        980                 985                 990

caa ggt cct agc ttg ctc att gac ctt cct gtt gtg gct caa agg agg   3141
Gln Gly Pro Ser Leu Leu Ile Asp Leu Pro Val Val Ala Gln Arg Arg
    995                1000                1005

gag caa gaa gat ttg cct tta tat caa cac caa gcg aca cga gtt att   3189
Glu Gln Glu Asp Leu Pro Leu Tyr Gln His Gln Ala Thr Arg Val Ile
1010                1015                1020                1025

tcc aag gcc tca gca tac aca gga atg ttg tct tct aga tat gcc act   3237
Ser Lys Ala Ser Ala Tyr Thr Gly Met Leu Ser Ser Arg Tyr Ala Thr
                1030                1035                1040

gat aca tgt gag tta cct gag aga gaa gaa ggc gaa gga gaa gaa act   3285
Asp Thr Cys Glu Leu Pro Glu Arg Glu Glu Gly Glu Gly Glu Glu Thr
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cca aat ttt agc cac tgg ggt cca ccg aga att gtt gag att ttt aga   3333
Pro Asn Phe Ser His Trp Gly Pro Pro Arg Ile Val Glu Ile Phe Arg
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gaa ccc aat gtg tct ctt ggg atc agt att gtt ggt gga caa act gtt   3381
Glu Pro Asn Val Ser Leu Gly Ile Ser Ile Val Gly Gly Gln Thr Val
   1075                1080                1085

ata aaa cgt cta aag aat gga gag gag ctt aaa ggt ata ttc atc aaa   3429
Ile Lys Arg Leu Lys Asn Gly Glu Glu Leu Lys Gly Ile Phe Ile Lys
1090                1095                1100                1105

caa gtt tta gaa gac agt cca gca ggg aag acg aac gca ctt aaa act   3477
Gln Val Leu Glu Asp Ser Pro Ala Gly Lys Thr Asn Ala Leu Lys Thr
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gga gat aaa ata ctt gag gtg tct gga gta gat ttg cag aat gcc tca   3525
Gly Asp Lys Ile Leu Glu Val Ser Gly Val Asp Leu Gln Asn Ala Ser
           1125                1130                1135

cac agc gaa gca gtt gag gcc att aag aat gca gga aac cct gtg gtg   3573
His Ser Glu Ala Val Glu Ala Ile Lys Asn Ala Gly Asn Pro Val Val
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ttc att gtt cag agt ttg tca tcc act cca cga gtc att cct aat gta   3621
Phe Ile Val Gln Ser Leu Ser Ser Thr Pro Arg Val Ile Pro Asn Val
   1155                1160                1165

cat aac aag gcc aac aaa atc acc agt aac cag aac cag gac acc caa   3669
His Asn Lys Ala Asn Lys Ile Thr Ser Asn Gln Asn Gln Asp Thr Gln
1170                1175                1180                1185

gaa aag aaa gaa aag agg caa gga act gct cca ccg cca atg aaa ctt   3717
Glu Lys Lys Glu Lys Arg Gln Gly Thr Ala Pro Pro Pro Met Lys Leu
               1190                1195                1200

cct cct cct tat aaa gct ctg act gat gac agt gat gaa aat gaa gaa   3765
Pro Pro Pro Tyr Lys Ala Leu Thr Asp Asp Ser Asp Glu Asn Glu Glu
           1205                1210                1215

gaa gat gcc ttt acc gac caa aaa atc aga caa aga tat gca gat ctg   3813
Glu Asp Ala Phe Thr Asp Gln Lys Ile Arg Gln Arg Tyr Ala Asp Leu
       1220                1225                1230

cct gga gaa ctg cac att att gaa ctt gaa aaa gat aag aat gga ctt   3861
Pro Gly Glu Leu His Ile Ile Glu Leu Glu Lys Asp Lys Asn Gly Leu
   1235                1240                1245

gga ctc agc ctt gct ggt aat aaa gac cga tca cgc atg agc ata ttt   3909
Gly Leu Ser Leu Ala Gly Asn Lys Asp Arg Ser Arg Met Ser Ile Phe
1250                1255                1260                1265

gtg gtg gga att aac ccg gaa gga cct gct gcc gca gat gga cga atg   3957
Val Val Gly Ile Asn Pro Glu Gly Pro Ala Ala Ala Asp Gly Arg Met
               1270                1275                1280

cat att gga gat gaa ctc tta gag ata aac aat cag att ctg tat gga   4005
His Ile Gly Asp Glu Leu Leu Glu Ile Asn Asn Gln Ile Leu Tyr Gly
           1285                1290                1295

aga agt cac caa aat gca tct gcc att att aag act gcc cca tca aag   4053
Arg Ser His Gln Asn Ala Ser Ala Ile Ile Lys Thr Ala Pro Ser Lys
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gtc aag ctg gtt ttc atc aga aac gag gat gca gtc aat cag atg gcc   4101
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gtt act ccc ttt cca gtg cca tca agt tct cca tct tct att gag gat   4149
Val Thr Pro Phe Pro Val Pro Ser Ser Ser Pro Ser Ser Ile Glu Asp
1330                1335                1340                1345

cag agc ggc acc gaa cct att agt agt gag gaa gat ggc agc ctc gaa   4197
Gln Ser Gly Thr Glu Pro Ile Ser Ser Glu Glu Asp Gly Ser Leu Glu
                1350                1355                1360

gtt ggt att aaa caa ttg cct gaa agt gaa agc ttc aaa ctg gct gtc   4245
Val Gly Ile Lys Gln Leu Pro Glu Ser Glu Ser Phe Lys Leu Ala Val
           1365                1370                1375

agc cag atg aaa cag caa aaa tat cca aca aaa gtc tcc ttc agt tca   4293
Ser Gln Met Lys Gln Gln Lys Tyr Pro Thr Lys Val Ser Phe Ser Ser
       1380                1385                1390

caa gag ata cca tta gca cca gct tca tca tac cat tca aca gat gca   4341
Gln Glu Ile Pro Leu Ala Pro Ala Ser Ser Tyr His Ser Thr Asp Ala
   1395                1400                1405

gac ttc aca ggc tat ggt ggt ttc cag gct cct ctg tca gtg gac ccc   4389
Asp Phe Thr Gly Tyr Gly Gly Phe Gln Ala Pro Leu Ser Val Asp Pro
1410                1415                1420                1425

gca acg tgt ccc att gtc cct gga cag gaa atg att ata gaa ata tcc   4437
Ala Thr Cys Pro Ile Val Pro Gly Gln Glu Met Ile Ile Glu Ile Ser
                1430                1435                1440

aag gga cgt tca ggg ctt ggt ctc agc att gtg gga gga aaa gac aca   4485
Lys Gly Arg Ser Gly Leu Gly Leu Ser Ile Val Gly Gly Lys Asp Thr
           1445                1450                1455

ccc ttg aat gct ata gtt atc cat gaa gtc tat gaa gaa ggg gca gca   4533
Pro Leu Asn Ala Ile Val Ile His Glu Val Tyr Glu Glu Gly Ala Ala
       1460                1465                1470

gcc aga gat gga aga ctt tgg gct ggt gac cag ata tta gag gtt aat   4581
Ala Arg Asp Gly Arg Leu Trp Ala Gly Asp Gln Ile Leu Glu Val Asn
   1475                1480                1485

ggg gtt gac ctg agg aac tcc agc cac gaa gaa gcc atc aca gcc ctg   4629
Gly Val Asp Leu Arg Asn Ser Ser His Glu Glu Ala Ile Thr Ala Leu
1490                1495                1500                1505

agg cag acc ccc cag aag gtg cgg ctg gtg gtg tat aga gat gaa gca   4677
Arg Gln Thr Pro Gln Lys Val Arg Leu Val Val Tyr Arg Asp Glu Ala
                1510                1515                1520

cac tac cgg gat gag gag aac ttg gag att ttc cct gtg gat ctg cag   4725
His Tyr Arg Asp Glu Glu Asn Leu Glu Ile Phe Pro Val Asp Leu Gln
           1525                1530                1535

aag aaa gct ggc cgg ggc ctg ggc ctg agc atc gtt ggg aaa cga aat   4773
Lys Lys Ala Gly Arg Gly Leu Gly Leu Ser Ile Val Gly Lys Arg Asn
       1540                1545                1550

gga agc gga gtg ttt att tct gac atc gtg aaa ggc gga gcc gca gac   4821
Gly Ser Gly Val Phe Ile Ser Asp Ile Val Lys Gly Gly Ala Ala Asp
   1555                1560                1565
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ctg gat ggg aga ttg att cag gga gat cag atc tta tct gtg aat ggg   4869
Leu Asp Gly Arg Leu Ile Gln Gly Asp Gln Ile Leu Ser Val Asn Gly
1570                1575                1580                1585

gag gac atg aga aat gcc tca cag gag aca gtg gcc acc atc ctc aag   4917
Glu Asp Met Arg Asn Ala Ser Gln Glu Thr Val Ala Thr Ile Leu Lys
                1590                1595                1600

tgt gca cag gga ctt gtg cag cta gag att gga aga ctc cga gct ggt   4965
Cys Ala Gln Gly Leu Val Gln Leu Glu Ile Gly Arg Leu Arg Ala Gly
            1605                1610                1615

tcc tgg acc tcc gca agg acg aca tca cag aac agt cag ggt agt cag   5013
Ser Trp Thr Ser Ala Arg Thr Thr Ser Gln Asn Ser Gln Gly Ser Gln
        1620                1625                1630

cag agt gca cac agc agc tgt cat ccc tcc ttc gct cct gtc atc act   5061
Gln Ser Ala His Ser Ser Cys His Pro Ser Phe Ala Pro Val Ile Thr
    1635                1640                1645

ggc ctg caa aac ctg gtt ggc aca aaa aga gtt tca gat cct tcc cag   5109
Gly Leu Gln Asn Leu Val Gly Thr Lys Arg Val Ser Asp Pro Ser Gln
1650                1655                1660                1665

aaa aat tca ggc aca gat atg gaa cca agg act gtt gag ata aac agg   5157
Lys Asn Ser Gly Thr Asp Met Glu Pro Arg Thr Val Glu Ile Asn Arg
                1670                1675                1680

gag ctc agt gat gcc ctt gga atc agt att gct gga gga aga gga agt   5205
Glu Leu Ser Asp Ala Leu Gly Ile Ser Ile Ala Gly Gly Arg Gly Ser
            1685                1690                1695

ccc tta gga gat atc ccc gta ttt att gcc atg att cag gct agc gga   5253
Pro Leu Gly Asp Ile Pro Val Phe Ile Ala Met Ile Gln Ala Ser Gly
        1700                1705                1710

gtg gcc gca cgg aca cag aag ctt aaa gtt gga gat cgg att gtc agc   5301
Val Ala Ala Arg Thr Gln Lys Leu Lys Val Gly Asp Arg Ile Val Ser
    1715                1720                1725

att aac ggg caa cct ttg gat ggg ctg tct cac gcg gat gtg gtt aat   5349
Ile Asn Gly Gln Pro Leu Asp Gly Leu Ser His Ala Asp Val Val Asn
1730                1735                1740                1745

ctg ctg aag aat gcc tac ggg cgc att atc ctg cag gtt gta gca gat   5397
Leu Leu Lys Asn Ala Tyr Gly Arg Ile Ile Leu Gln Val Val Ala Asp
                1750                1755                1760

acc aat ata agc gcc ata gca gct cag ctt gaa aac atg tct aca ggc   5445
Thr Asn Ile Ser Ala Ile Ala Ala Gln Leu Glu Asn Met Ser Thr Gly
            1765                1770                1775

tac cac ctt ggt tcg ccc act gct gaa cac cat cca gaa gac aca gaa   5493
Tyr His Leu Gly Ser Pro Thr Ala Glu His His Pro Glu Asp Thr Glu
        1780                1785                1790

aca cct cca cct aag att att act ttg gag aaa ggc tct gaa ggc ttg   5541
Thr Pro Pro Pro Lys Ile Ile Thr Leu Glu Lys Gly Ser Glu Gly Leu
    1795                1800                1805

ggg ttt agt att gta ggg ggt tat gga agt ccc cat gga gac ctg cca   5589
Gly Phe Ser Ile Val Gly Gly Tyr Gly Ser Pro His Gly Asp Leu Pro
1810                1815                1820                1825
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att tat gtc aag act gta ttt gca aag gga gca gct gca gat gac ggc   5637
Ile Tyr Val Lys Thr Val Phe Ala Lys Gly Ala Ala Ala Asp Asp Gly
                1830                1835                1840

cga tta aaa cga ggg gat cag att tta gct gtt aat ggc gag acc ctg   5685
Arg Leu Lys Arg Gly Asp Gln Ile Leu Ala Val Asn Gly Glu Thr Leu
            1845                1850                1855

gaa ggt gtt act cat gag caa gca gtc gcc att cta aaa cac cag aga   5733
Glu Gly Val Thr His Glu Gln Ala Val Ala Ile Leu Lys His Gln Arg
        1860                1865                1870

ggg act gta acc tta act gtg ctg tcatgagcct cgggcctgat cacaagatag  5787
Gly Thr Val Thr Leu Thr Val Leu
    1875                1880

atgttgttgt ttagaatatc cacaggcaga tgaagttctg agtgggtat             5836
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<210> 3
<211> 1881
<212> PRT
<213> Homo sapiens

<400> 3

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Met Pro Glu Asn Pro Ala Thr Asp Lys Leu Gln Val Leu Gln Val Leu
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Asp Arg Leu Lys Met Lys Leu Gln Glu Lys Gly Asp Thr Ser Gln Asn
             20                  25                  30

Glu Lys Leu Ser Met Phe Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn
         35                  40                  45

Gln Ile Leu Thr Leu Gln Gln Ser Ile Lys Gln Leu Lys Gly Gln Leu
     50                  55                  60

Asn His Ile Pro Ser Asp Cys Ser Ala Asn Phe Asp Phe Ser Arg Lys
 65                  70                  75                  80

Gly Leu Leu Val Phe Thr Asp Gly Ser Ile Thr Asn Gly Asn Val His
                 85                  90                  95

Arg Pro Ser Asn Asn Ser Thr Val Ser Gly Leu Phe Pro Trp Thr Pro
            100                 105                 110

Lys Leu Gly Asn Glu Asp Phe Asn Ser Val Ile Gln Gln Met Ala Gln
        115                 120                 125

Gly Arg Gln Ile Glu Tyr Ile Asp Ile Glu Arg Pro Ser Thr Gly Gly
    130                 135                 140

Leu Gly Phe Ser Val Val Ala Leu Arg Ser Gln Asn Leu Gly Lys Val
145                 150                 155                 160

Asp Ile Phe Val Lys Asp Val Gln Pro Gly Ser Val Ala Asp Arg Asp
                165                 170                 175

Gln Arg Leu Lys Glu Asn Asp Gln Ile Leu Ala Ile Asn His Thr Pro
            180                 185                 190

Leu Asp Gln Asn Ile Ser His Gln Gln Ala Ile Ala Leu Leu Gln Gln
        195                 200                 205
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Thr Thr Gly Ser Leu Arg Leu Ile Val Ala Arg Glu Pro Val His Thr
    210                 215                 220

Lys Ser Ser Thr Ser Ser Ser Leu Asn Asp Thr Thr Leu Pro Glu Thr
225                 230                 235                 240

Val Cys Trp Gly His Val Glu Glu Val Glu Leu Ile Asn Asp Gly Ser
                245                 250                 255

Gly Leu Gly Phe Gly Ile Val Gly Gly Lys Thr Ser Gly Val Val Val
            260                 265                 270

Arg Thr Ile Val Pro Gly Gly Leu Ala Asp Arg Asp Gly Arg Leu Gln
        275                 280                 285

Thr Gly Asp His Ile Leu Lys Ile Gly Gly Thr Asn Val Gln Gly Met
    290                 295                 300

Thr Ser Glu Gln Val Ala Gln Val Leu Arg Asn Cys Gly Asn Ser Val
305                 310                 315                 320

Arg Met Leu Val Ala Arg Asp Pro Ala Gly Asp Ile Ser Val Thr Pro
                325                 330                 335

Pro Ala Pro Ala Ala Leu Pro Val Ala Leu Pro Thr Val Ala Ser Lys
            340                 345                 350

Gly Pro Gly Ser Asp Ser Ser Leu Phe Glu Thr Tyr Asn Val Glu Leu
        355                 360                 365

Val Arg Lys Asp Gly Gln Ser Leu Gly Ile Arg Ile Val Gly Tyr Val
    370                 375                 380

Gly Thr Ser His Thr Gly Glu Ala Ser Gly Ile Tyr Val Lys Ser Val
385                 390                 395                 400

Ile Pro Gly Ser Ala Ala Tyr His Asn Gly His Ile Gln Val Asn Asp
                405                 410                 415

Lys Ile Val Ala Val Asp Gly Val Asn Ile Gln Gly Phe Ala Asn His
            420                 425                 430

Asp Val Val Glu Val Leu Arg Asn Ala Gly Gln Val Val His Leu Thr
        435                 440                 445

Leu Val Arg Arg Lys Thr Ser Ser Ser Thr Ser Pro Leu Glu Pro Pro
    450                 455                 460

Ser Asp Arg Gly Thr Val Val Glu Pro Leu Lys Pro Pro Ala Leu Phe
465                 470                 475                 480

Leu Thr Gly Ala Val Glu Thr Glu Thr Asn Val Asp Gly Glu Asp Glu
                485                 490                 495

Glu Ile Lys Glu Arg Ile Asp Thr Leu Lys Asn Asp Asn Ile Gln Ala
            500                 505                 510

Leu Glu Lys Leu Glu Lys Val Pro Asp Ser Pro Glu Asn Glu Leu Lys
        515                 520                 525

Ser Arg Trp Glu Asn Leu Leu Gly Pro Asp Tyr Glu Val Met Val Ala
    530                 535                 540
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Thr Leu Asp Thr Gln Ile Ala Asp Asp Ala Glu Leu Gln Lys Tyr Ser
545 550 555 560

Lys Leu Leu Pro Ile His Thr Leu Arg Leu Gly Val Glu Val Asp Ser
565 570 575

Phe Asp Gly His His Tyr Ile Ser Ser Ile Val Ser Gly Gly Pro Val
580 585 590

Asp Thr Leu Gly Leu Leu Gln Pro Glu Asp Glu Leu Leu Glu Val Asn
595 600 605

Gly Met Gln Leu Tyr Gly Lys Ser Arg Arg Glu Ala Val Ser Phe Leu
610 615 620

Lys Glu Val Pro Pro Pro Phe Thr Leu Val Cys Cys Arg Arg Leu Phe
625 630 635 640

Asp Asp Glu Ala Ser Val Asp Glu Pro Arg Arg Thr Glu Thr Ser Leu
645 650 655

Pro Glu Thr Glu Val Asp His Asn Met Asp Val Asn Thr Glu Glu Asp
660 665 670

Asp Asp Gly Glu Leu Ala Leu Trp Ser Pro Glu Val Lys Ile Val Glu
675 680 685

Leu Val Lys Asp Cys Lys Gly Leu Gly Phe Ser Ile Leu Asp Tyr Gln
690 695 700

Asp Pro Leu Asp Pro Thr Arg Ser Val Ile Val Ile Arg Ser Leu Val
705 710 715 720

Ala Asp Gly Val Ala Glu Arg Ser Gly Gly Leu Leu Pro Gly Asp Arg
725 730 735

Leu Val Ser Val Asn Glu Tyr Cys Leu Asp Asn Thr Ser Leu Ala Glu
740 745 750

Ala Val Glu Ile Leu Lys Ala Val Pro Pro Gly Leu Val His Leu Gly
755 760 765

Ile Cys Lys Pro Leu Val Glu Asp Asn Glu Glu Glu Ser Cys Tyr Ile
770 775 780

Leu His Ser Ser Ser Asn Glu Asp Lys Thr Glu Phe Ser Gly Thr Ile
785 790 795 800

His Asp Ile Asn Ser Ser Leu Ile Leu Glu Ala Pro Lys Gly Phe Arg
805 810 815

Asp Glu Pro Tyr Phe Lys Glu Glu Leu Val Asp Glu Pro Phe Leu Asp
820 825 830

Leu Gly Lys Ser Phe His Ser Gln Gln Lys Glu Ile Glu Gln Ser Lys
835 840 845

Glu Ala Trp Glu Met His Glu Phe Leu Thr Pro Arg Leu Gln Glu Met
850 855 860

Asp Glu Glu Arg Glu Met Leu Val Asp Glu Glu Tyr Glu Leu Tyr Gln
865 870 875 880

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Asp Pro Ser Pro Ser Met Glu Leu Tyr Pro Leu Ser His Ile Gln Glu
                885                 890                 895

Ala Thr Pro Val Pro Ser Val Asn Glu Leu His Phe Gly Thr Gln Trp
            900                 905                 910

Leu His Asp Asn Glu Pro Ser Glu Ser Gln Glu Ala Arg Thr Gly Arg
        915                 920                 925

Thr Val Tyr Ser Gln Glu Ala Gln Pro Tyr Gly Tyr Cys Pro Glu Asn
    930                 935                 940

Val Met Lys Glu Asn Phe Val Met Glu Ser Leu Pro Ser Val Pro Ser
945                 950                 955                 960

Thr Glu Gly Asn Ser Gln Gln Gly Arg Phe Asp Asp Leu Glu Asn Leu
                965                 970                 975

Asn Ser Leu Ala Lys Thr Ser Leu Asp Leu Gly Met Ile Pro Asn Asp
            980                 985                 990

Val Gln Gly Pro Ser Leu Leu Ile Asp Leu Pro Val Val Ala Gln Arg
        995                1000                1005

Arg Glu Gln Glu Asp Leu Pro Leu Tyr Gln His Gln Ala Thr Arg Val
    1010                1015                1020

Ile Ser Lys Ala Ser Ala Tyr Thr Gly Met Leu Ser Ser Arg Tyr Ala
025                1030                1035                1040

Thr Asp Thr Cys Glu Leu Pro Glu Arg Glu Glu Gly Glu Gly Glu Glu
                1045                1050                1055

Thr Pro Asn Phe Ser His Trp Gly Pro Pro Arg Ile Val Glu Ile Phe
            1060                1065                1070

Arg Glu Pro Asn Val Ser Leu Gly Ile Ser Ile Val Gly Gly Gln Thr
        1075                1080                1085

Val Ile Lys Arg Leu Lys Asn Gly Glu Glu Leu Lys Gly Ile Phe Ile
    1090                1095                1100

Lys Gln Val Leu Glu Asp Ser Pro Ala Gly Lys Thr Asn Ala Leu Lys
105                1110                1115                1120

Thr Gly Asp Lys Ile Leu Glu Val Ser Gly Val Asp Leu Gln Asn Ala
                1125                1130                1135

Ser His Ser Glu Ala Val Glu Ala Ile Lys Asn Ala Gly Asn Pro Val
            1140                1145                1150

Val Phe Ile Val Gln Ser Leu Ser Ser Thr Pro Arg Val Ile Pro Asn
        1155                1160                1165

Val His Asn Lys Ala Asn Lys Ile Thr Ser Asn Gln Asn Gln Asp Thr
    1170                1175                1180

Gln Glu Lys Lys Glu Lys Arg Gln Gly Thr Ala Pro Pro Pro Met Lys
185                1190                1195                1200

Leu Pro Pro Pro Tyr Lys Ala Leu Thr Asp Asp Ser Asp Glu Asn Glu
                1205                1210                1215
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Glu Glu Asp Ala Phe Thr Asp Gln Lys Ile Arg Gln Arg Tyr Ala Asp
1220 1225 1230

Leu Pro Gly Glu Leu His Ile Ile Glu Leu Glu Lys Asp Lys Asn Gly
1235 1240 1245

Leu Gly Leu Ser Leu Ala Gly Asn Lys Asp Arg Ser Arg Met Ser Ile
1250 1255 1260

Phe Val Val Gly Ile Asn Pro Glu Gly Pro Ala Ala Ala Asp Gly Arg
265 1270 1275 1280

Met His Ile Gly Asp Glu Leu Leu Glu Ile Asn Asn Gln Ile Leu Tyr
1285 1290 1295

Gly Arg Ser His Gln Asn Ala Ser Ala Ile Ile Lys Thr Ala Pro Ser
1300 1305 1310

Lys Val Lys Leu Val Phe Ile Arg Asn Glu Asp Ala Val Asn Gln Met
1315 1320 1325

Ala Val Thr Pro Phe Pro Val Pro Ser Ser Ser Pro Ser Ser Ile Glu
1330 1335 1340

Asp Gln Ser Gly Thr Glu Pro Ile Ser Ser Glu Glu Asp Gly Ser Leu
345 1350 1355 1360

Glu Val Gly Ile Lys Gln Leu Pro Glu Ser Glu Ser Phe Lys Leu Ala
1365 1370 1375

Val Ser Gln Met Lys Gln Gln Lys Tyr Pro Thr Lys Val Ser Phe Ser
1380 1385 1390

Ser Gln Glu Ile Pro Leu Ala Pro Ala Ser Ser Tyr His Ser Thr Asp
1395 1400 1405

Ala Asp Phe Thr Gly Tyr Gly Gly Phe Gln Ala Pro Leu Ser Val Asp
1410 1415 1420

Pro Ala Thr Cys Pro Ile Val Pro Gly Gln Glu Met Ile Ile Glu Ile
425 1430 1435 1440

Ser Lys Gly Arg Ser Gly Leu Gly Leu Ser Ile Val Gly Gly Lys Asp
1445 1450 1455

Thr Pro Leu Asn Ala Ile Val Ile His Glu Val Tyr Glu Glu Gly Ala
1460 1465 1470

Ala Ala Arg Asp Gly Arg Leu Trp Ala Gly Asp Gln Ile Leu Glu Val
1475 1480 1485

Asn Gly Val Asp Leu Arg Asn Ser Ser His Glu Glu Ala Ile Thr Ala
1490 1495 1500

Leu Arg Gln Thr Pro Gln Lys Val Arg Leu Val Val Tyr Arg Asp Glu
505 1510 1515 1520

Ala His Tyr Arg Asp Glu Glu Asn Leu Glu Ile Phe Pro Val Asp Leu
1525 1530 1535

Gln Lys Lys Ala Gly Arg Gly Leu Gly Leu Ser Ile Val Gly Lys Arg
1540 1545 1550

Asn Gly Ser Gly Val Phe Ile Ser Asp Ile Val Lys Gly Gly Ala Ala
1555 1560 1565

Asp Leu Asp Gly Arg Leu Ile Gln Gly Asp Gln Ile Leu Ser Val Asn
1570 1575 1580

Gly Glu Asp Met Arg Asn Ala Ser Gln Glu Thr Val Ala Thr Ile Leu
585 1590 1595 1600

Lys Cys Ala Gln Gly Leu Val Gln Leu Glu Ile Gly Arg Leu Arg Ala
1605 1610 1615

Gly Ser Trp Thr Ser Ala Arg Thr Thr Ser Gln Asn Ser Gln Gly Ser
1620 1625 1630

Gln Gln Ser Ala His Ser Ser Cys His Pro Ser Phe Ala Pro Val Ile
1635 1640 1645

Thr Gly Leu Gln Asn Leu Val Gly Thr Lys Arg Val Ser Asp Pro Ser
1650 1655 1660

Gln Lys Asn Ser Gly Thr Asp Met Glu Pro Arg Thr Val Glu Ile Asn
665 1670 1675 1680

Arg Glu Leu Ser Asp Ala Leu Gly Ile Ser Ile Ala Gly Gly Arg Gly
1685 1690 1695

Ser Pro Leu Gly Asp Ile Pro Val Phe Ile Ala Met Ile Gln Ala Ser
1700 1705 1710

Gly Val Ala Ala Arg Thr Gln Lys Leu Lys Val Gly Asp Arg Ile Val
1715 1720 1725

Ser Ile Asn Gly Gln Pro Leu Asp Gly Leu Ser His Ala Asp Val Val
1730 1735 1740

Asn Leu Leu Lys Asn Ala Tyr Gly Arg Ile Ile Leu Gln Val Val Ala
745 1750 1755 1760

Asp Thr Asn Ile Ser Ala Ile Ala Ala Gln Leu Glu Asn Met Ser Thr
1765 1770 1775

Gly Tyr His Leu Gly Ser Pro Thr Ala Glu His His Pro Glu Asp Thr
1780 1785 1790

Glu Thr Pro Pro Pro Lys Ile Ile Thr Leu Glu Lys Gly Ser Glu Gly
1795 1800 1805

Leu Gly Phe Ser Ile Val Gly Gly Tyr Gly Ser Pro His Gly Asp Leu
1810 1815 1820

Pro Ile Tyr Val Lys Thr Val Phe Ala Lys Gly Ala Ala Ala Asp Asp
825 1830 1835 1840

Gly Arg Leu Lys Arg Gly Asp Gln Ile Leu Ala Val Asn Gly Glu Thr
1845 1850 1855

Leu Glu Gly Val Thr His Glu Gln Ala Val Ala Ile Leu Lys His Gln
1860 1865 1870

Arg Gly Thr Val Thr Leu Thr Val Leu
1875 1880

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<213> Mus musculus

<220>
<221> CDS
<222> (105)..(290)

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gcccgatcag acttttgga agtgattgaa aagaatatcc caaa atg cct gaa aac 116
Met Pro Glu Asn
1

cct gct gca gag aag atg cag gtc ctg cag gtc ctg gat cgc ctt cga 164
Pro Ala Ala Glu Lys Met Gln Val Leu Gln Val Leu Asp Arg Leu Arg
5 10 15 20

ggg aag ctg cag gag aag gga gac acg acg cag aac gag aag ctg tct 212
Gly Lys Leu Gln Glu Lys Gly Asp Thr Thr Gln Asn Glu Lys Leu Ser
25 30 35

gcg ttc tac gag acg ctg aag agc cct ctc ttc aac cag atc ctt aca 260
Ala Phe Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn Gln Ile Leu Thr
40 45 50

ctg cag cag tcc atc aag cag ctg aag gga 290
Leu Gln Gln Ser Ile Lys Gln Leu Lys Gly
55 60

<210> 5
<211> 62
<212> PRT
<213> Mus musculus

<400> 5
Met Pro Glu Asn Pro Ala Ala Glu Lys Met Gln Val Leu Gln Val Leu
1 5 10 15

Asp Arg Leu Arg Gly Lys Leu Gln Glu Lys Gly Asp Thr Thr Gln Asn
20 25 30

Glu Lys Leu Ser Ala Phe Tyr Glu Thr Leu Lys Ser Pro Leu Phe Asn
35 40 45

Gln Ile Leu Thr Leu Gln Gln Ser Ile Lys Gln Leu Lys Gly
50 55 60

<210> 6
<211> 15
<212> PRT
<213> Homo sapiens

<400> 6
Asn Glu Pro Phe Asp Glu Asp Gln His Thr Gln Ile Thr Lys Val
1 5 10 15

<210> 7
<211> 16

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:SH3 Binding Protein PDZ Domain

<400> 7
Ser Gly Ser Gly Ile Leu Ala Pro Pro Val Pro Pro Arg Asn Thr Arg
1 5 10 15

<210> 8
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:AF6 PDZ Binding Protein

<400> 8
Ser Gly Asp Asp Gly Asp Asp Pro Phe Leu Gln Tyr Glu Phe Tyr Val
1 5 10 15

<210> 9
<211> 16
<212> PRT
<213> Homo sapiens

<400> 9
Glu Asn Glu Pro Phe Asp Glu Asp Gln His Thr Gln Ile Thr Lys Val
1 5 10 15

<210> 10
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MMSC1 Primers

<400> 10
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<210> 11
<211> 22
<212> DNA
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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 11
ctacagtagg cagggcaaca gg 22

<210> 12
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MMSC1 Primers

<400> 12
gttttcccag tcacgacgcg ggctcccacc tgctcctc 38

<210> 13
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<212> DNA
<213> Artificial Sequence

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<400> 13
aggaaacagc tatgaccatg tgaacactaa caaacctttc c 41

<210> 14
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<400> 14
gttttcccag tcacgacgtc aactcaacca tataccctca 40

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aggaaacagc tatgaccatg gctggacatc cttcacgaag 40

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<400> 16
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aggaaacagc tatgaccatc cccaacaaac tgtttcaggc 40

<210> 18
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gttttcccag tcacgacgcc agggaaccag tccacaca 38

<210> 19
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<212> DNA
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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 19
aggaaacagc tatgaccatc ctgactgaat tcccacag 38

<210> 20
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<212> DNA
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<400> 20
tcctggagga ttagcagatc gag 23

<210> 21
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MMSC1 Primers

<400> 21
ggtaatccaa aatgctgaat ccca 24

<210> 22
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<212> DNA
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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 22
gttttcccag tcacgacgaa gattggtggc acaaacgtg 39

<210> 23

<211> 41
<212> DNA
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<400> 23
aggaaacagc tatgaccata gcactgccag gtattatact t 41

<210> 24
<211> 41
<212> DNA
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<400> 24
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<210> 25
<211> 41
<212> DNA
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<210> 26
<211> 39
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gttttcccag tcacgacgac atcctcatct acttctcca 39

<210> 27
<211> 40
<212> DNA
<213> Artificial Sequence

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<210> 28
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<212> DNA
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gttttcccag tcacgacggg aaaacctgtt gggtcctg 38

<210> 29
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
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<400> 29
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<210> 30
<211> 22
<212> DNA
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<400> 30
gtggattcct ttgatgggca cc 22

<210> 31
<211> 23
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<400> 31
ctttgagcca caacaggaag gtc 23

<210> 32
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:MMSC1 Primers

<400> 32
gttttcccag tcacgacgtg agctgcttga ggtcaatgg 39

<210> 33
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<400> 33

aggaaacagc tatgaccatc taaagggtcc tggtaatcc 39

<210> 34
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<220>
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<212> DNA
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<210> 36
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<400> 36
gttttcccag tcacgacgga aatattgaaa gctgtgcc 38

<210> 37
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<212> DNA
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<220>
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<400> 37
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<210> 38
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<400> 38
gttttcccag tcacgacgaa agtctttcca ttcccaacaa 40

<210> 39

<211> 39
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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 39
aggaaacagc tatgaccatc catacggctg tgcctcctg 39

<210> 40
<211> 25
<212> DNA
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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 40
gagttatatc aagatccctc accat 25

<210> 41
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<212> DNA
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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 41
caaatatgct catgcgtgat cgg 23

<210> 42
<211> 41
<212> DNA
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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 42
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<210> 43
<211> 40
<212> DNA
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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 43
aggaaacagc tatgaccata aatcttcttg ctcccctcctt 40

<210> 44
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<400> 44
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<210> 45
<211> 40
<212> DNA
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<223> Description of Artificial Sequence:MMSC1 Primers

<400> 45
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<210> 46
<211> 38
<212> DNA
<213> Artificial Sequence

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<400> 46
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<210> 47
<211> 41
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<400> 47
aggaaacagc tatgaccata ctcgtggagt ggatgacaaa c 41

<210> 48
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 48
gttttcccag tcacgacgca gttgaggcca ttaagaat 38

<210> 49
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<400> 49

aggaaacagc tatgaccatc aagttcaata atgtgcagtt ct 42

<210> 50
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<400> 50
cgccaatgaa acttcctcct cct 23

<210> 51
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tctcctgtga ggcatttctc atg 23

<210> 52
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<212> DNA
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<210> 53
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<212> DNA
<213> Artificial Sequence

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<223> Description of Artificial Sequence:MMSC1 Primers

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aggaaacagc tatgaccatc tgattgactg catcctcg 38

<210> 54
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<210> 55

<211> 41
<212> DNA
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<220>
<223> Description of Artificial Sequence:MMSC1 Primers

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aggaaacagc tatgaccatg tgaagtctgc atctgttgaa t 41

<210> 56
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
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<210> 57
<211> 40
<212> DNA
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<220>
<223> Description of Artificial Sequence:MMSC1 Primers

<400> 57
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<210> 58
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<223> Description of Artificial Sequence:MMSC1 Primers

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<210> 59
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<400> 63
aggaaacagc tatgaccata accaggtttt gcaggccagt 40

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gttttcccag tcacgacgtc agggtagtca gcagagtgc 39

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<400> 65

aggaaacagc tatgaccatt acccacatcc gcgtgagac 39